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Input file T198sHVEM1; Output File T198sHVEM1.pat
Sequence length 1929

GTCGACCCACGCGTCCGCTCGGCTTTGCCTGGACAGCTCCTGCCTCCCGCAGGGCCCACCTGTGTCCCCCAGCGCCGCT  79

CCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGGCA  158

CAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGCAATGGCGCTGAGTT  237

                                                        M   E   P   P   G     5
CCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGC ATG GAG CCT CCT GGA  311

 D   W   G   P   P   P   W   R   S   T   P   R   T   D   V   L   R   L   V   L    25
GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG  371

 Y   L   T   F   L   G   A   P   C   Y   A   P   A   L   P   S   C   K   E   D    45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC  431

 E   Y   P   V   G   S   E   C   C   P   K   C   S   P   G   Y   R   V   K   E    65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG  491

 A   C   G   E   L   T   G   T   V   C   E   P   C   P   P   G   T   Y   I   A    85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC  551

 H   L   N   G   L   S   K   C   L   Q   C   Q   M   C   D   P   A   M   G   L   105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG  611

 R   A   S   R   N   C   S   R   T   E   N   A   V   C   G   C   S   P   G   H   125
CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC  671

 F   C   I   V   Q   D   G   D   H   C   A   A   C   R   A   Y   A   T   S   S   145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC  731

 P   G   Q   R   V   Q   K   G   G   T   E   S   Q   D   T   L   C   Q   N   C   165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC  791

 P   P   G   T   F   S   P   N   G   T   L   E   E   C   Q   H   Q   T   N   R   185
CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA  851

 A   W   K   S   Q   T   D   L   *                                               194
GCT TGG AAA AGT CAG ACA GAC CTC TGA                                             878

GGTCTCATCCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGG  957

CTCCCTGAGGCTGAGTGAACACTGGGCGCTGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGG  1036

CTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCA  1115

TTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTC  1194

CATCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACG  1273

GTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCC  1352

AGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCC  1431

GCCCTGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGC  1510

CATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCC  1589

AGTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCG  1668

CGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTG  1747

TGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGA  1826

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Figure 1

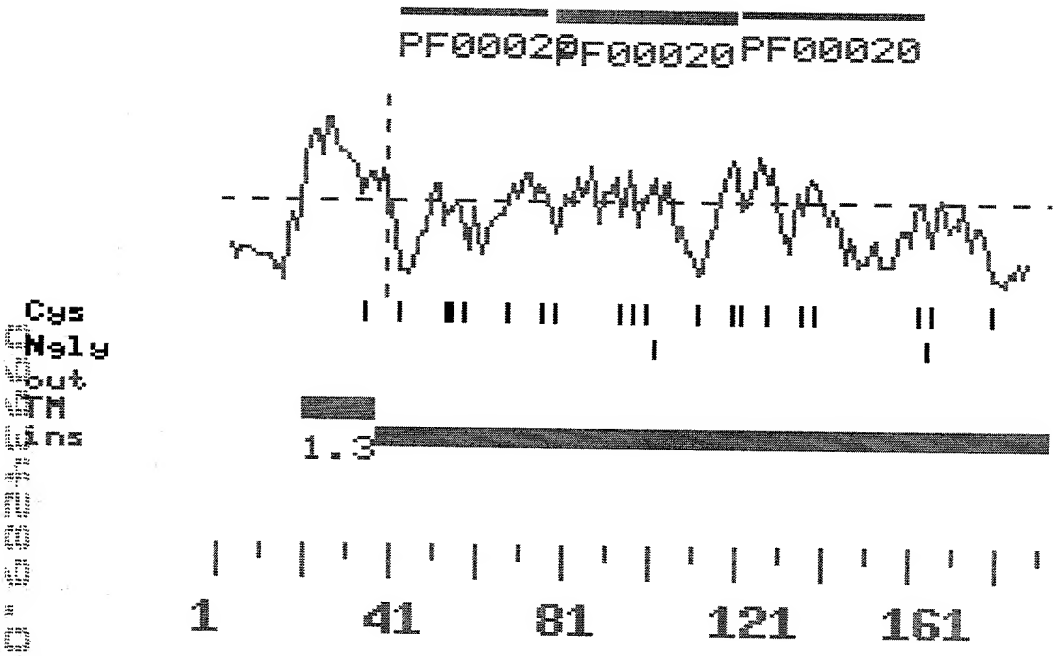

Figure 2

Input file T198sHVEM2; Output File T198sHVEM2.pat
Sequence length 1596

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 S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC  205

 C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC  265

 C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA  325

 V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT  385

 L   Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG  445

 T   E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   133
ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC  505

 H   C   A   A   C   R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   153
CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA  565

 G   T   E   S   Q   D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   173
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT  625

 G   T   L   E   E   C   Q   H   Q   T   N   W   P   N   H   M   C   E   K   K   193
GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAT TGG CCT AAT CAT ATG TGT GAA AAG AAG  685

 K   A   K   G   *
AAA GCC AAG GGG TGA                                                              198
                                                                                 700

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GTCTCCATCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCA  937

CCACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCG 1016

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CGTGCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGA 1253

GCGCCAGTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGT 1332

CTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTG 1411

CAGTGTGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGT 1490

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Figure 3

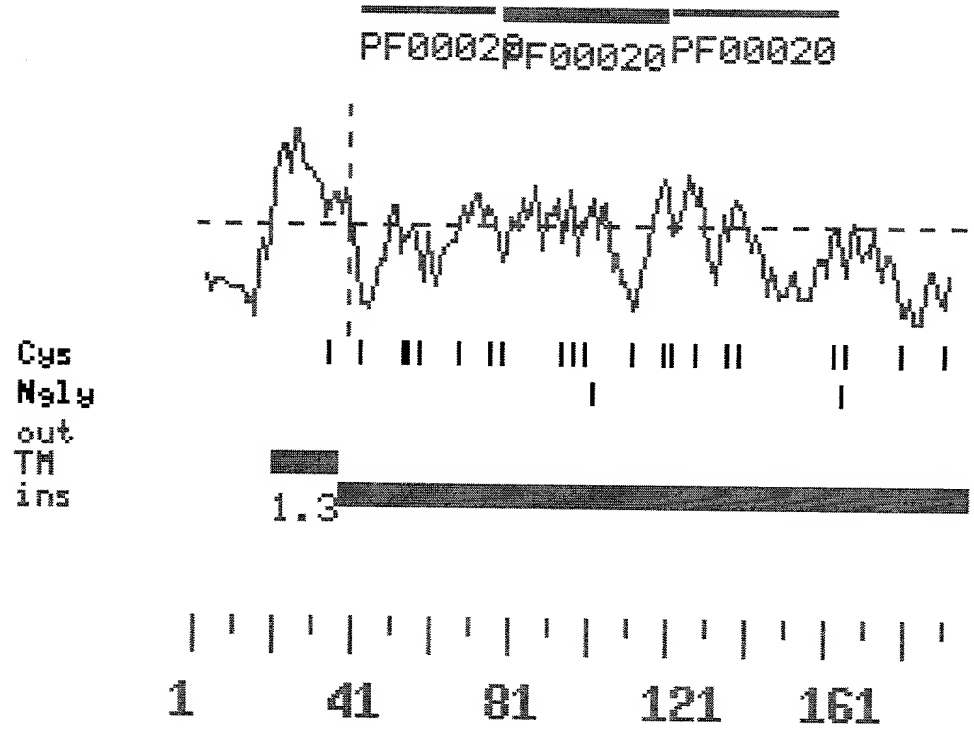

Figure 4

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Input file sHVEM3; Output File sHVEM3.pat
Sequence length 2313

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GAGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC     138

 D   V   S   R   L   V   L   Y   L   T   F   L   G   A   P   C   Y   A   P   A    38
GAC GTC TCG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT   198

 L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C   P   K   C   S    58
CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT   258

 P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   V   C   E   P   C    78
CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC   318

 P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   L   Q   C   Q   M    98
CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG   378

 C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   T   E   N   A   V   118
TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG   438

 C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   H   C   A   A   C   138
TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC   498

 R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   G   T   E   S   Q   158
CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG   558

 D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   T   L   E   E   178
GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA   618

 C   Q   H   Q   T   K   K   A   *                                               187
TGT CAG CAC CAG ACC AAA AAG GCT TGA                                             645

AGGTCCCACCCTGAGCGGCACCCTGGTCACATGCCTGCGTCCAGGAGAGCTGCAGGGCTGAAGCCTGTGTGCCCCAGAT  724
AACCCCTTCCATGGGCCCAGACAAAGCCTCATCAGATCTGAGCTTCCTGGAGGCTCAGGATGGGCCTTCCCAGAAGCAG  803
GCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAATGTCAGGGCCATGGGAGGGCC  882
CCTGGGCTTCAGGGGTTGGGGAAAGTGAACACTCTGCTCTTTGTCCACCTTCGGGAGGACACCTTCAAATGCTGACCCT  961
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Figure 5

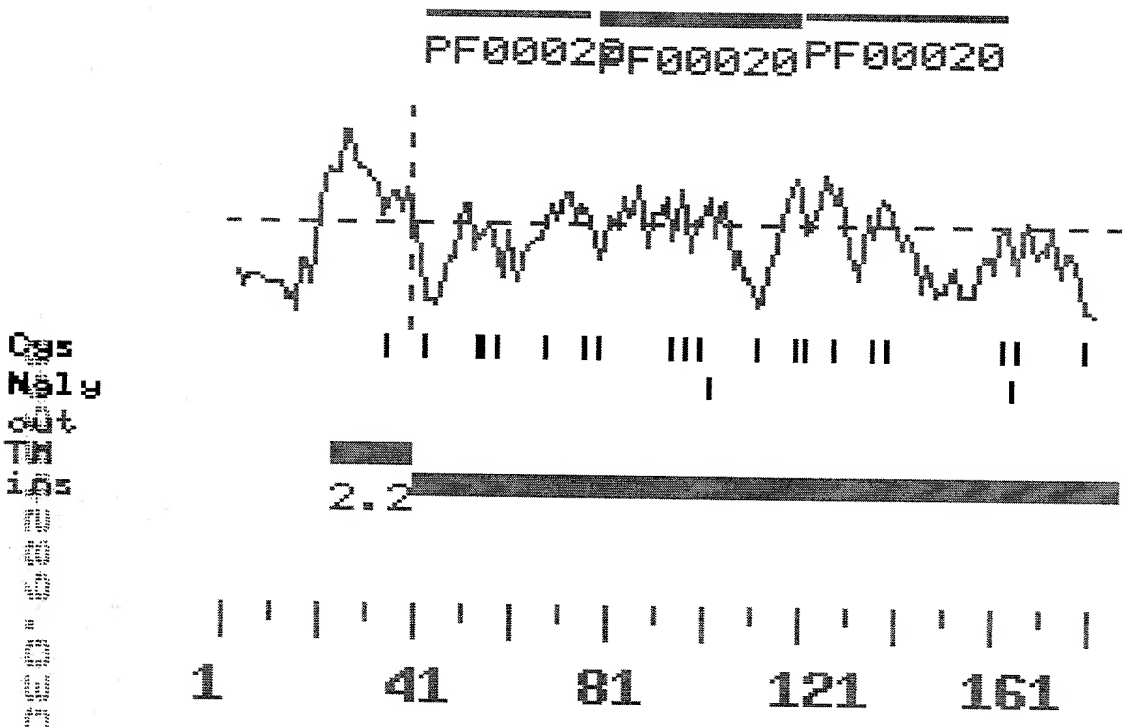

Figure 6

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 T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   C    34
ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC   204

 Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C    54
TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC   264

 P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   V    74
CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG   324

 C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   L    94
TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG   384

 Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   T   114
CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA   444

 E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   H   134
GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC   504

 C   A   A   C   R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   G   154
TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC   564

 T   E   S   Q   D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   174
ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG   624

 T   L   E   E   C   Q   H   Q   T   K   C   S   W   L   V   T   K   A   G   A   194
ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC AGC TGG CTG GTG ACG AAG GCC GGA GCT   684

 G   T   S   S   S   H   W   V   W   W   F   L   S   G   S   L   V   I   V   I   214
GGG ACC AGC AGC TCC CAC TGG GTA TGG TGG TTT CTC TCA GGG AGC CTC GTC ATC GTC ATT   744

 V   C   S   T   V   G   L   I   I   C   V   K   R   R   K   P   R   G   D   V   234
GTT TGC TCC ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT GTA   804

 V   K   V   I   V   S   V   Q   V   L   I   L   L   P   L   S   L   P   P   P   254
GTC AAG GTG ATC GTC TCC GTC CAG GTA TTG ATC CTC CTC CCC CTC TCC CTC CCC CCT CCA   864

 P   S   H   L   P   S   P   R   W   G   W   C   F   W   C   T   W   W   G   L   274
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 P   V   L   *                                                                   278
CCA GTT CTC TGA                                                                  936

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Figure 7

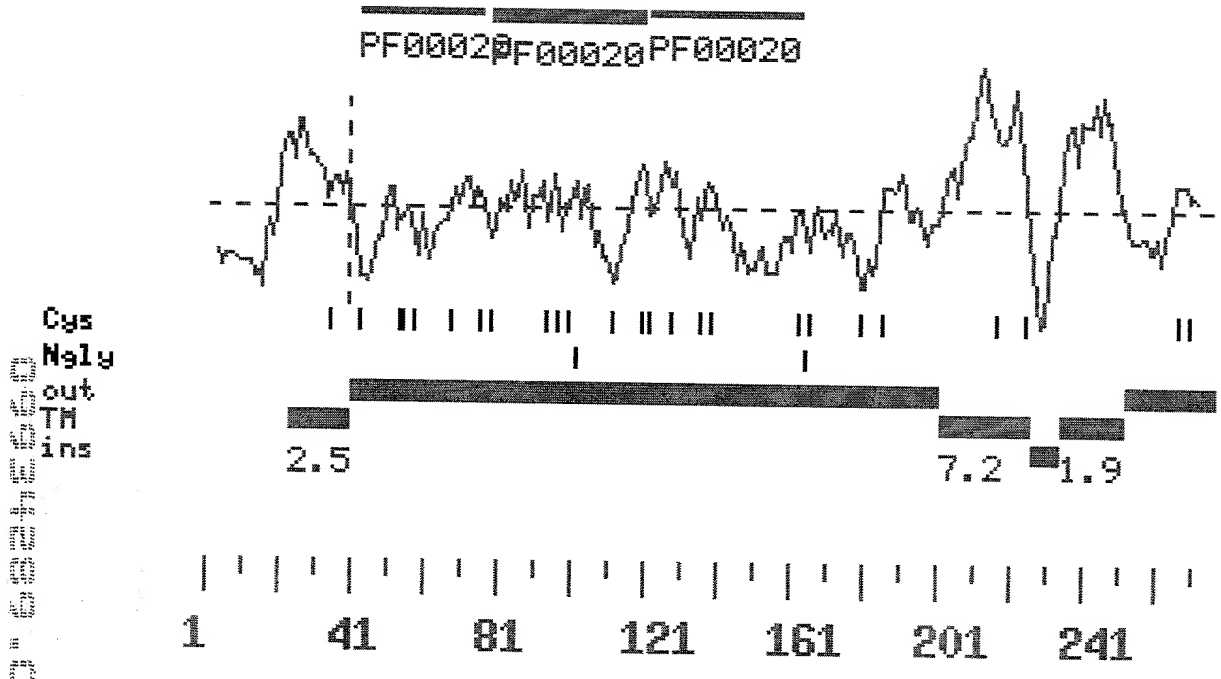
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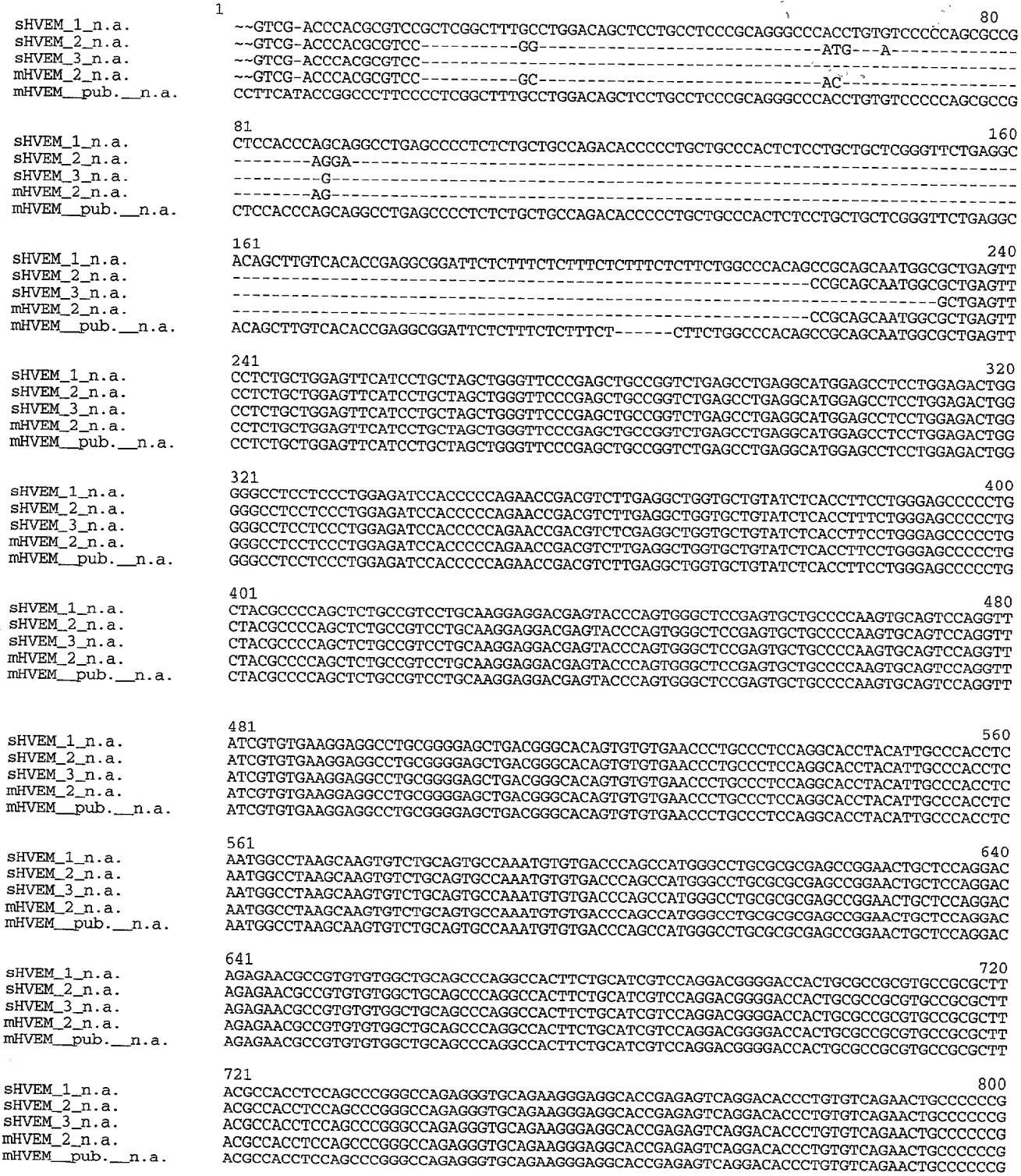
Figure 8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560
561
640
641
720
721
800

Figure 9A

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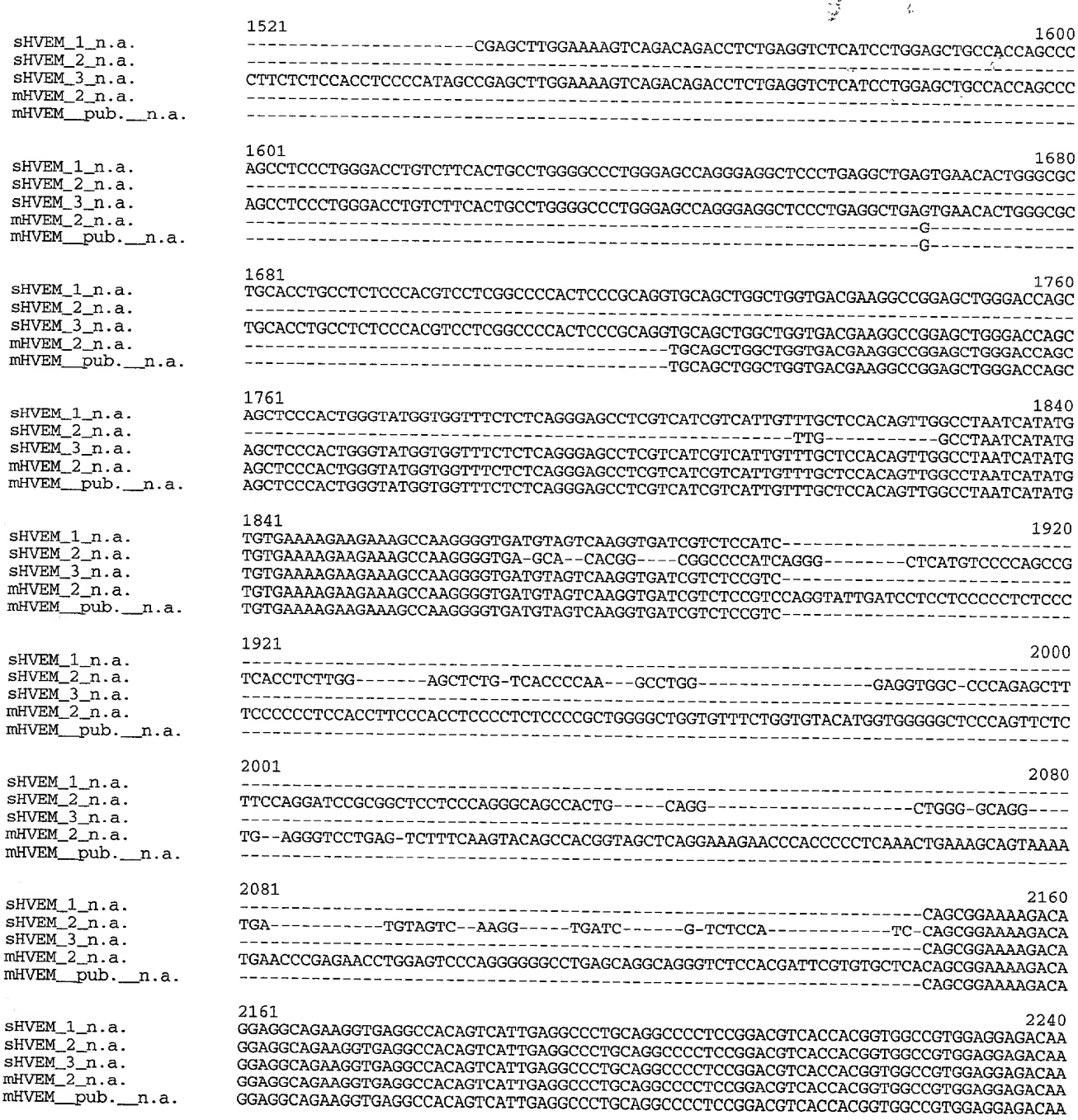
Figure 9B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sHVEM_2_n.a. ----------
sHVEM_3_n.a. CTTCTCTCCACCTCCCCATAGCCGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCC
mHVEM_2_n.a. ----------
mHVEM__pub.__n.a. ----------
1601 1680
sHVEM_1_n.a. AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC
sHVEM_2_n.a. ----------
sHVEM_3_n.a. AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC
mHVEM_2_n.a. ----------G----------
mHVEM__pub.__n.a. ----------G----------
1681 1760
sHVEM_1_n.a. TGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
sHVEM_2_n.a. ----------
sHVEM_3_n.a. TGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
mHVEM_2_n.a. ----------TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
mHVEM__pub.__n.a. ----------TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
1761 1840
sHVEM_1_n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
sHVEM_2_n.a. ----------TTG----------GCCTAATCATATG
sHVEM_3_n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
mHVEM_2_n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
mHVEM__pub.__n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
1841 1920
sHVEM_1_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC----------
sHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGA-GCA--CACGG----CGGCCCCATCAGGG--------CTCATGTCCCCAGCCG
sHVEM_3_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC----------
mHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCCTCTCCC
mHVEM__pub.__n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC----------
1921 2000
sHVEM_1_n.a. ----------
sHVEM_2_n.a. TCACCTCTTGG-------AGCTCTG-TCACCCCAA---GCCTGG----------GAGGTGGC-CCCAGAGCTT
sHVEM_3_n.a. ----------
mHVEM_2_n.a. TCCCCCCTCCACCTTCCCACCTCCCCTCTCCCCGCTGGGGCTGGTGTTTCTGGTGTACATGGTGGGGGCTCCCAGTTCTC
mHVEM__pub.__n.a. ----------
2001 2080
sHVEM_1_n.a. ----------
sHVEM_2_n.a. TTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTG-----CAGG----------CTGGG-GCAGG----
sHVEM_3_n.a. ----------
mHVEM_2_n.a. TG--AGGGTCCTGAG-TCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCCACCCCCTCAAACTGAAAGCAGTAAAA
mHVEM__pub.__n.a. ----------
2081 2160
sHVEM_1_n.a. ----------CAGCGGAAAAGACA
sHVEM_2_n.a. TGA----------TGTAGTC--AAGG-----TGATC------G-TCTCCA----------TC-CAGCGGAAAAGACA
sHVEM_3_n.a. ----------CAGCGGAAAAGACA
mHVEM_2_n.a. TGAACCCGAGAACCTGGAGTCCCAGGGGGGCCTGAGCAGGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGAAAAGACA
mHVEM__pub.__n.a. ----------CAGCGGAAAAGACA
2161 2240
sHVEM_1_n.a. GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA
sHVEM_2_n.a. GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA
sHVEM_3_n.a. GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA
mHVEM_2_n.a. GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA
mHVEM__pub.__n.a. GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA

Figure 9C

```
                    2241                                                                                                2320
sHVEM_1_n.a.        TACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG
sHVEM_2_n.a.        TACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG
sHVEM_3_n.a.        TACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG
mHVEM_2_n.a.        TACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG
mHVEM__pub.__n.a.   TACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG

                    2321                                                                                                2400
sHVEM_1_n.a.        CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT
sHVEM_2_n.a.        CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT
sHVEM_3_n.a.        CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT
mHVEM_2_n.a.        CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT
mHVEM__pub.__n.a.   CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT

                    2401                                                                                                2480
sHVEM_1_n.a.        CCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG
sHVEM_2_n.a.        CCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG
sHVEM_3_n.a.        CCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG
mHVEM_2_n.a.        CCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG
mHVEM__pub.__n.a.   CCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG

                    2481                                                                                                2560
sHVEM_1_n.a.        CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCA
sHVEM_2_n.a.        CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCA
sHVEM_3_n.a.        CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCA
mHVEM_2_n.a.        CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCA
mHVEM__pub.__n.a.   CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCA

                    2561                                                                                                2640
sHVEM_1_n.a.        CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA
sHVEM_2_n.a.        CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA
sHVEM_3_n.a.        CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA
mHVEM_2_n.a.        CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA
mHVEM__pub.__n.a.   CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA

                    2641                                                                                                2720
sHVEM_1_n.a.        GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGG
sHVEM_2_n.a.        GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGG
sHVEM_3_n.a.        GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGG
mHVEM_2_n.a.        GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGG
mHVEM__pub.__n.a.   GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGG

                    2721                                                                                                2800
sHVEM_1_n.a.        AAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG
sHVEM_2_n.a.        AAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG
sHVEM_3_n.a.        AAGTGATTTTCTAAATTGGATTTGAATTCGG----------------------------------------------------
mHVEM_2_n.a.        AAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG
mHVEM__pub.__n.a.   AAGTGATTTTCTAAATTGGATTTGAATTCCGGTCCTGTCTTCTATTTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG

                    2801                                                                                                2880
sHVEM_1_n.a.        GGAGGATGTAAATATCTTGTTTCTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA---
sHVEM_2_n.a.        GGAGGATGTAAATATCTTGTTTCTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA---
sHVEM_3_n.a.        ----------------------------------AAAAAAAAAAAAAAAAAAAAA----------------------------
mHVEM_2_n.a.        GGAGGATGTAAATATCTTGTTTCTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
mHVEM__pub.__n.a.   GGAGGATGTAAATATCTTGTTTCTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAA----------------------------

                    2881                                                                                                2904
sHVEM_1_n.a.        ------------------------
sHVEM_2_n.a.        ------------------------
sHVEM_3_n.a.        --------------GGGCGGCCGC
mHVEM_2_n.a.        AAAAAAAAAAAAAAGGGCGGCCGC
mHVEM__pub.__n.a.   ------------------------
```

Figure 9D

```
                    1                                                                                80
sHVEM_1_a.a.        MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP
sHVEM_2_a.a.        MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP
sHVEM_3_a.a.        MEPPGDWGPPPWRSTPRTDVSRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP
mHVEM_2_a.a.        MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP
mHVEM__pub.__a.a.   MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP

                    81                                                                               160
sHVEM_1_a.a.        GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT
sHVEM_2_a.a.        GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT
sHVEM_3_a.a.        GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT
mHVEM_2_a.a.        GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT
mHVEM__pub.__a.a.   GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT

                    161                                                                              240
sHVEM_1_a.a.        LCQNCPPGTFSPNGTLEECQHQTNRAWKSQTDL----------------------------------------------
sHVEM_2_a.a.        LCQNCPPGTFSPNGTLEECQHQTNWPNHMCEKKKAKG------------------------------------------
sHVEM_3_a.a.        LCQNCPPGTFSPNGTLEECQHQTKKA-----------------------------------------------------
mHVEM_2_a.a.        LCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
mHVEM__pub.__a.a.   LCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS

                    241                                                                              283
sHVEM_1_a.a.        ------------------------------------------
sHVEM_2_a.a.        ------------------------------------------
sHVEM_3_a.a.        ------------------------------------------
mHVEM_2_a.a.        VQVLILLPLSLPPPPSHLPSPRWGWCFWCTWWGLPVL------
mHVEM__pub.__a.a.   VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
```

Figure 10